

#6

# CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/506,308

CRF Edit Date: 9/13/04  
Edited by: KE

Realigned nucleic acid/amino acid numbers/text, in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

**ENTERED**

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: ☒ invalid beginning/end-of-file text ; ☐ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other:



PCT

## RAW SEQUENCE LISTING

DATE: 09/13/2004

PATENT APPLICATION: US/10/506,308

TIME: 10:52:23

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\09132004\J506308.raw

```

2 <110> APPLICANT: NAKANISHI, Atsushi
3   HIKICHI, Yukiko
4   UNO, Yumiko
6 <120> TITLE OF INVENTION: Novel Protein and its DNA
8 <130> FILE REFERENCE: 3030 USOP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/506,308
C--> 10 <141> CURRENT FILING DATE: 2004-09-01
10 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02564
11 <151> PRIOR FILING DATE: 2003-03-05
13 <150> PRIOR APPLICATION NUMBER: JP 2002-061133
14 <151> PRIOR FILING DATE: 2002-03-06
16 <150> PRIOR APPLICATION NUMBER: JP 2002-098852
17 <151> PRIOR FILING DATE: 2002-04-01
19 <150> PRIOR APPLICATION NUMBER: JP 2002-184883
20 <151> PRIOR FILING DATE: 2002-06-25
22 <160> NUMBER OF SEQ ID NOS: 84
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 724
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
30 Met Lys Ser Ala Lys Gly Ile Glu Asn Leu Ala Phe Val Pro Ser Ser
31           5              10              15
32 Pro Asp Ile Leu Arg Arg Leu Ser Ala Ser Pro Ser Gln Ile Glu Val
33           20              25              30
34 Ser Ala Leu Ser Ser Asp Pro Gln Arg Glu Asn Ser Gln Pro Gln Glu
35           35              40              45
36 Leu Gln Lys Pro Gln Glu Pro Gln Lys Ser Pro Glu Pro Ser Leu Pro
37           50              55              60
38 Ser Ala Pro Pro Asn Val Ser Glu Glu Lys Leu Arg Ser Leu Ser Leu
39 65           70              75              80
40 Ser Glu Phe Glu Glu Gly Ser Tyr Gly Trp Arg Asn Phe His Pro Gln
41           85              90              95
42 Cys Leu Gln Arg Cys Asn Thr Pro Gly Gly Phe Leu Leu His Tyr Cys
43           100             105             110
44 Leu Leu Ala Val Thr Gln Gly Ile Val Val Asn Gly Leu Val Asn Ile
45           115             120             125
46 Ser Ile Ser Thr Val Glu Lys Arg Tyr Glu Met Lys Ser Ser Leu Thr
47           130             135             140
48 Gly Leu Ile Ser Ser Ser Tyr Asp Ile Ser Phe Cys Leu Leu Ser Leu
49 145           150             155             160
50 Phe Val Ser Phe Phe Gly Glu Arg Gly His Lys Pro Arg Trp Leu Ala
51           165             170             175

```

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```

52 Phe Ala Ala Phe Met Ile Gly Leu Gly Ala Leu Val Phe Ser Leu Pro
53      180      185      190
54 Gln Phe Phe Ser Gly Glu Tyr Lys Leu Gly Ser Leu Phe Glu Asp Thr
55      195      200      205
56 Cys Val Thr Thr Arg Asn Ser Thr Ser Cys Thr Ser Ser Thr Ser Ser
57      210      215      220
58 Leu Ser Asn Tyr Leu Tyr Val Phe Ile Leu Gly Gln Leu Leu Leu Gly
59 225      230      235      240
60 Ala Gly Gly Thr Pro Leu Tyr Thr Leu Gly Thr Ala Phe Leu Asp Asp
61      245      250      255
62 Ser Val Pro Thr His Lys Ser Ser Leu Tyr Ile Gly Thr Gly Tyr Ala
63      260      265      270
64 Met Ser Ile Leu Gly Pro Ala Ile Gly Tyr Val Leu Gly Gly Gln Leu
65      275      280      285
66 Leu Thr Ile Tyr Ile Asp Val Ala Met Gly Glu Ser Thr Asp Val Thr
67      290      295      300
68 Glu Asp Asp Pro Arg Trp Leu Gly Ala Trp Trp Ile Gly Phe Leu Leu
69 305      310      315      320
70 Ser Trp Ile Phe Ala Trp Ser Leu Ile Ile Pro Phe Ser Cys Phe Pro
71      325      330      335
72 Lys His Leu Pro Gly Thr Ala Glu Ile Gln Ala Gly Lys Thr Ser Gln
73      340      345      350
74 Ala His Gln Ser Asn Ser Asn Ala Asp Val Lys Phe Gly Lys Ser Ile
75      355      360      365
76 Lys Asp Phe Pro Ala Ala Leu Lys Asn Leu Met Lys Asn Ala Val Phe
77      370      375      380
78 Met Cys Leu Val Leu Ser Thr Ser Ser Glu Ala Leu Ile Thr Thr Gly
79 385      390      395      400
80 Phe Ala Thr Phe Leu Pro Lys Phe Ile Glu Asn Gln Phe Gly Leu Thr
81      405      410      415
82 Ser Ser Phe Ala Ala Thr Leu Gly Gly Ala Val Leu Ile Pro Gly Ala
83      420      425      430
84 Ala Leu Gly Gln Ile Leu Gly Gly Phe Leu Val Ser Lys Phe Arg Met
85      435      440      445
86 Thr Cys Lys Asn Thr Met Lys Phe Ala Leu Phe Thr Ser Gly Val Ala
87      450      455      460
88 Leu Thr Leu Ser Phe Val Phe Met Tyr Ala Lys Cys Glu Asn Glu Pro
89 465      470      475      480
90 Phe Ala Gly Val Ser Glu Ser Tyr Asn Gly Thr Gly Glu Leu Gly Asn
91      485      490      495
92 Leu Ile Ala Pro Cys Asn Ala Asn Cys Asn Cys Ser Arg Ser Tyr Tyr
93      500      505      510
94 Tyr Pro Val Cys Gly Asp Gly Val Gln Tyr Phe Ser Pro Cys Phe Ala
95      515      520      525
96 Gly Cys Ser Asn Pro Val Ala His Arg Lys Pro Lys Val Tyr Tyr Asn
97      530      535      540
98 Cys Ser Cys Ile Glu Arg Lys Thr Glu Ile Thr Ser Thr Ala Glu Thr
99 545      550      555      560
100 Phe Gly Phe Glu Ala Lys Ala Gly Lys Cys Glu Thr His Cys Ala Lys

```

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```

101          565          570          575
102 Leu Pro Ile Phe Leu Cys Ile Phe Phe Ile Val Ile Ile Phe Thr Phe
103          580          585          590
104 Met Ala Gly Thr Pro Ile Thr Val Ser Ile Leu Arg Cys Val Asn His
105          595          600          605
106 Arg Gln Arg Ser Leu Ala Leu Gly Ile Gln Phe Met Val Leu Arg Leu
107          610          615          620
108 Leu Gly Thr Ile Pro Gly Pro Ile Ile Phe Gly Phe Thr Ile Asp Ser
109 625          630          635          640
110 Thr Cys Ile Leu Trp Asp Ile Asn Asp Cys Gly Ile Lys Gly Ala Cys
111          645          650          655
112 Trp Ile Tyr Asp Asn Ile Lys Met Ala His Met Leu Val Ala Ile Ser
113          660          665          670
114 Val Thr Cys Lys Val Ile Thr Met Phe Phe Asn Gly Phe Ala Ile Phe
115          675          680          685
116 Leu Tyr Lys Pro Pro Pro Ser Ala Thr Asp Val Ser Phe His Lys Glu
117          690          695          700
118 Asn Ala Val Val Thr Asn Val Leu Ala Glu Gln Asp Leu Asn Lys Ile
119 705          710          715          720
120 Val Lys Glu Gly
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 2172
124 <212> TYPE: DNA
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 2
128 atgaagagcg ccaaagggtat tgagaacttg gcttttgtcc cctccagccc agacatcctg 60
129 cgccgcttgt ctgcgtcgcc ctcccaaadc gaagtctctg ccttgtcctc tgaccccaa 120
130 agagagaatt ctcagccaca ggagcttcag aagccccagg agccccagaa gtcacccgag 180
131 ccatctctgc cttcagcccc tccaatgtc tccgaagaga agctccggtc actgtcgctg 240
132 tccgagtttg aggaggggtc ttacggctgg aggaacttcc atcctcaatg tctccagcgc 300
133 tgcaacacac ctggaggctt tctgcttcac tactgcctct tggccgtcac gcaaggattt 360
134 gtagttaatg gcctagtaaa tattagcatt tccactgttg agaagcgta tgaaatgaag 420
135 agttccctga ctggcctgat ttcataaagc tacgatattt cattctgttt gttgtcttta 480
136 tttgtatcat tctttggtga aagaggacat aagccgagat ggcttgcatt tgcagccttt 540
137 atgattggac tgggagcact tgtattctca ttgccacaat ttttcagtgg agaataaaa 600
138 ttgggggtctc tttttgaaga cacttgtgtg acaacaagga atagcaccag ttgtacatct 660
139 tcaacttctt cactttctaa ctacttgtat gtcttcatct tgggacaact attgctgggg 720
140 gcaggaggaa ctctcttta tactctggga acagcctttc ttgatgattc tgtgccca 780
141 cacaagtctt ctctctatat aggaaccggt tatgctatgt caatcttagg ccctgctatt 840
142 ggctatgtat tgggaggaca actgctaacc atatacattg atgttgctat gggagaaaagc 900
143 actgatgtca ctgaggatga tccgcgatgg ttgggagctt ggtggattgg gtttcttcta 960
144 tcatggatct ttgcttggtc ttttaataata cctttttctt gctttccaaa acatttacca 1020
145 ggtacagcag aaattcaagc tggaaaaaact tcccaggctc atcagagtaa tagtaatgca 1080
146 gatgtgaaat ttggaaaaag tattaaagat tttccagctg ctctaaaagaa tttgatgaag 1140
147 aatgctgtct ttatgtgttt agttctatca acttcttcag aagccttaat tactactgga 1200
148 tttgctacat ttttacctaa atttatagaa aatcaattcg gattgacatc cagcttcgca 1260
149 gctactcttg gaggggctgt ttttaattcct ggagctgctc tcggtcaaat tttaggtggc 1320
150 ttccttgttt caaaattcag aatgacatgt aaaaacacaa tgaagtttgc actgttcaca 1380
151 tctggagttg cacttacgct gagttttgta tttatgtatg ccaaagtga aaatgagcca 1440

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152 tttgctggtg tatctgaatc atataatggg actggagaat tgggaaactt gatagcccct 1500
153 tgtaatgccca attgtaactg ttcgcgatca tattattatc ctgtctgtgg agatggagtc 1560
154 caatattttt ctccctgctt tgcaggctgt tcaaaccagag ttgcacacag gaagccaaag 1620
155 gtatattaca actgttcctg tattgaaaagg aaaacagaaa taacatccac tgcagaaaact 1680
156 tttggttttg aagctaaaagc tggaaaatgt gaaactcatt gtgcgaaact gcccatattc 1740
157 ctttgcattt tctttattgt aattattttt acctttatgg ccggtactcc tataactgtg 1800
158 tctatcctaa ggtgtgttaa tcacagacaa cgggccctag ccttggggaat acaatttatg 1860
159 gtccttcgat tattaggaac aattcctgga ccaattatat ttggtttcac aatagacagc 1920
160 acatgtattc tttgggatat aaatgattgt ggaattaaag gagcttgctg gatttatgat 1980
161 aacatcaaga tggcccatat gctagtagcc ataagtgtta cttgtaaagt tatcaccatg 2040
162 ttcttcaatg gatttgcaat ctttttgat aaaccacctc catcagccac agatgtgtca 2100
163 tttcataaag agaatgcagt tgtgactaat gtttttagcag aacaggatct caacaaaata 2160
164 gtaaaagaag gg 2172
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 27
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer
174 <400> SEQUENCE: 3
175 ccataccta acgactcact atagggc 27
177 <210> SEQ ID NO: 4
178 <211> LENGTH: 26
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Primer
185 <400> SEQUENCE: 4
186 aaacccaatc caccaagctc ccaacc 26
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 23
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Primer
196 <400> SEQUENCE: 5
197 actcactata gggctcgagc ggc 23
199 <210> SEQ ID NO: 6
200 <211> LENGTH: 25
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Primer
207 <400> SEQUENCE: 6
208 ccaatccacc aagctcccaa ccatc 25
210 <210> SEQ ID NO: 7
211 <211> LENGTH: 28
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence

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```

215 <220> FEATURE:
216 <223> OTHER INFORMATION: Primer
218 <400> SEQUENCE: 7
219 gttcctccag ccgtaagacc cctcctca                28
221 <210> SEQ ID NO: 8
222 <211> LENGTH: 25
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Primer
229 <400> SEQUENCE: 8
230 cggagacatt gggaggggct gaagg                25
232 <210> SEQ ID NO: 9
233 <211> LENGTH: 28
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Primer
240 <400> SEQUENCE: 9
241 ttgggagctt ggtggattgg gtttcttc                28
243 <210> SEQ ID NO: 10
244 <211> LENGTH: 29
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Primer
251 <400> SEQUENCE: 10
252 gggactggag aattgggaaa cttgatagc                29
254 <210> SEQ ID NO: 11
255 <211> LENGTH: 20
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Primer
262 <400> SEQUENCE: 11
263 cacgggggcg ctgtcacctg                20
265 <210> SEQ ID NO: 12
266 <211> LENGTH: 25
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Primer
273 <400> SEQUENCE: 12
274 atcgaggtaa attttccagg tgtaa                25
276 <210> SEQ ID NO: 13
277 <211> LENGTH: 23
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:

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**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/506,308**

DATE: 09/13/2004

TIME: 10:52:24

Input Set : **A:\pto.kd.txt**

Output Set: **N:\CRF4\09132004\J506308.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date